

SEQUENCE SUBMISSION

SEQ ID NO: 1 is mouse 499E9 nucleic acid sequence.

SEQ ID NO: 2 is mouse 499E9 amino acid sequence.

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(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.
Mattson, Jeanine D.

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(ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related Reagents

(iii) NUMBER OF SEQUENCES: 2

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 12-DEC-1997
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,846
(B) FILING DATE: 13-DEC-1996

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0686

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196
(B) TELEFAX: (650)496-1200

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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/62121-2968680

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 125..1072

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG 60
 TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CCGGGCGCCG 120
 CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG 169
 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
 1 5 10 15
 GAG GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC 217
 Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
 20 25 30
 CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC 265
 Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg
 35 40 45
 TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC 313
 Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys
 50 55 60
 AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA 361
 Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
 65 70 75
 ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT 409
 Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
 80 85 90 95
 GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA 457
 Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
 100 105 110
 CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG 505
 Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125
 AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA 553
 Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro
 130 135 140
 GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT 601
 Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro
 145 150 155

	GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA	649
	Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
	160 165 170 175	
5	TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC	697
	Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
	180 185 190	
10	TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT	745
	Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
	195 200 205	
15	AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT	793
	Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	
	210 215 220	
20	CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG	841
	His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
	225 230 235	
25	TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG	889
	Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
	240 245 250 255	
30	AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT	937
	Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
	260 265 270	
35	TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA	985
	Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
	275 280 285	
40	ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT	1033
	Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
	290 295 300	
45	GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT	1082
	Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
	305 310 315	
50	TTCGTGGAAC ATTAGCATGG ATGTCCTAGA TGTTTGGAAC CTTCCTAAAA AATGGATGAT	1142
	GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCACG GTGTATGAAA CTCACAGCCC	1202
55	TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTCAT	1262
	GGTGATTACA CAACGGTTTT ACAATTTTGT AATGATTTCC TAAGAATTGA ACCAGATTGG	1322
	GAGAGGTATT CCGATGCTTA TGAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC	1382
	TCTGGGTCTA ACCCCTGGAC ATGTGCCACT GAGAACCTTG AAATTAAGAA GATGCCATGT	1442
	CATTGCAAAG AAATGATAGT GTGAAGGGTT AAGTTCTTTT GAATTGTTAC ATTGCGCTGG	1502
	GACCTGCAAA TAAGTTCTTT TTTTCTAATG AGGAGAGAAA AATATATGTA TTTTATATA	1562

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	ATGTCTAAAG	TTATATTTCA	GGTGTAATGT	TTTCTGTGCA	AAGTTTTGTA	AATTATATTT	1622
5	GTGCTATAGT	ATTTGATTCA	AAATATTTAA	AAATGTCTCA	CTGTTGACAT	ATTTAATGTT	1682
	TTAAATGTAC	AGATGTATTT	AACTGGTGCA	CTTTGTAATT	CCCCTGAAGG	TACTCGTAGC	1742
	TAAGGGGGCA	GAATACTGTT	TCTGGTGACC	ACATGTAGTT	TATTTCTTTA	TTCTTTTTTAA	1802
10	CTTAATAGAG	TCTTCAGACT	TGTCAAACT	ATGCAAGCAA	AATAAATAAA	TAAAAATAAA	1862
	ATGAATATCT	TGAATAATAA	GTAGGATGTT	GGTCACCAGG	TGCCTTTCAA	ATTTAGAAGC	1922
15	TAATTGACTT	TAGGAGCTGA	CATAGCCAAA	AAGGATACAT	AATAGGCTAC	TGAAAATCTG	1982
	TCAGGAGTAT	TTATGCAATT	ATTGAACAGG	TGTCTTTTTT	TACAAGAGCT	ACAAATTGTA	2042
	AATTTTGTTT	CTTTTTTTTC	CCATAGAAAA	TGTACTATAG	TTTATCAGCC	AAAAACAAT	2102
20	CCACTTTTTA	ATTTAGTGAA	AGTTATTTTA	TTATACTGTA	CAATAAAAAGC	ATTGTTTCTG	2162
	AATGGCATTT	TTTGGTACTT	AAAAATGGC				2191

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
1 5 10 15

40 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
20 25 30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
35 40 45

45 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65 70 75 80

50 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
85 90 95

55 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
100 105 110

	Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	
			115					120					125				
5	Glu	Leu	Gln	His	Ile	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	
		130					135					140					
	Met	Met	Glu	Gly	Ser	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	
10	145					150					155					160	
	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	
					165					170					175		
	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	
15				180					185					190			
	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	
			195					200					205				
20	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	
		210					215					220					
	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	
25	225					230					235					240	
	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	
					245					250					255		
	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	
30				260					265					270			
	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile	
			275					280					285				
35	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala	
		290					295					300					
	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp					
40	305					310					315						

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